SEQUENCE LISTING

(1) GENERAL INFORMATION: (i) APPLICANT: (A) NAME: Hoechst Aktiengesellschaft, (B) STREET: -(C) CITY: Frankfurt (D) FEDERAL STATE: -(E) COUNTRY: Germany (F) POSTAL CODE: 65926 (G) TELEPHONE: 069-305-3005 (H) TELEFAX: 069-35-7175 (I) TELEX: 41234700 ho d (ii) TITLE OF APPLICATION: Dictyocaulus viviparus Antigen zur Diagnose des Lungenwurmbefalls/und zur Vakzinierung [Dictyocaulus viviparus antigen for the diagnosis of lungworm infestation and for vaccination] (iii) NUMBER OF SEQUENCES:/30 (iv) COMPUTER-READABLE FORM: (A) MEDIUM TYPE: /Floppy disk (B) COMPUTER: IFM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: /PatentIn Release #1.0, Version #1.25 (EPO) (2) INFORMATION FOR SEQ ID NO: 1: (i) SEQUENCE CHARACTERISTICS: Lī (A) LENGTH: 7 Amino acids (B) TYPE / Amino acid (C) STRANDEDNESS: Single (D) TOPØLOGY: linear (ii) MOLECULÉ TYPE: Protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: Ser Glu \$er Leu Tyr Glu Lys (2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 Amino acids (B) TYPE: Amino acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein (i★) FEATURES: (A) NAME/KEY: Protein (B) LOCATION: 1..7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Met Asp Asn Phe Val Lys 1 5

- (2) INFORMATION FOR SEQ ID NO: 3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..14
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Tyr Lys Asp Glu Asn Glu Phe Met Asp Ala Leu Lys Gln Lys 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..20
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Tyr Asp Ile Pro Glu Gln Tyr Arg Glu Ile Ile Pro Gln Asn Val Ala

10 15

Glu His Leu Lys 20

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein

of one or to be an arranged

- (B) LOCATION: 1..26
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asp Ala Ile Glu Lys Tyr Glu Asp Ile Pro Glu Gln Tyr Arg Glu Ile

Ile Pro Gln Asn Val Ala Glu His Leu Lys

- (2) INFORMATION FOR SEQ ID NO: 6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..18
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Phe His Ala Glu Leu Leu Ala Gly Ile Lys Pro Ser Leu Glu Glu Leu 10

Lys Lys

- (2) INFORMATION FOR SEQ ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 Amino acids

 - (B) TYPE: Amino acid
 (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..14
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Gln Phe Pro Ile Leu Thr Ser Val Phe Ser Asn Glu Glu Lys

- (2) INFORMATION FOR SEQ ID NO: 8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 Base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear

	(11)	MOLECULE TYPE: DNA (genomic)	
	(ix)	FEATURES: (A) NAME/KEY: exon (B) LOCATION: 121	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
TCN	GARUC	NY TNTAYGARAA R	21
(2)	TATEO	DMITTON FOR ORD IN 112	
(2)	INFO	RMATION FOR SEQ ID NO: 9:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(ix)	FEATURES: (A) NAME/KEY: exon (B) LOCATION: 121	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
ATG	ATGGA	YA AYTTYGTNAA R	21
(2)	INFO	RMATION FOR SEQ ID NO: 10:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(ix)	FEATURES: (A) NAME/KEY: exon (B) LOCATION: 142	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
TAYA	AARGA	YG ARAAYGARTT YATGGAYGCN YTNAARCARA AR	42
(2)	INFO	RMATION FOR SEQ ID NO: 11:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	

	(ix)	FEATURES: (A) NAME/KEY: exon (B) LOCATION: 160	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
TAYO	GAYAT:	HC CNGARCARTA YMGNGARATH ATHCCNCARA AYGTNGCNGA RCAYYTNAAR	60
(2)	INFO	RMATION FOR SEQ ID NO: 12:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
,	(ix)	FEATURES: (A) NAME/KEY: exon (B) LOCATION: 178	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
GAYO	GCNAT:	HG ARAARTAYGA RGAYATHCCN GARCARTAYM GNGARATHAT HCCNCARAAY	60
GTNO	GCNGA:	RC AYYTNAAR	78
(2)	INFO	RMATION FOR SEQ ID NO: 13:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(ix)	FEATURES: (A) NAME/KEY: exon (B) LOCATION: 154	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
TTYC	CAYGC	NG ARYTNYTNGC NGGNATHAAR CCNTCNYTNG ARGARYTNAA RAAR	54
(2)	INFO	RMATION FOR SEQ ID NO: 14:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
		FEATURES: (A) NAME/KEY: exon	

(B) LOCATION: 1..42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CARTTYCCNA THYTNACNTC NGTNTTYTCN AAYGARGARA AR

42

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 Base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURES:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1..29
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: CCGGAATTCG AYGCNATNGA RAARTAYGA

29

- (2) INFORMATION FOR SEQ ID NO: 16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..7
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ala Ile Glu Lys Tyr Glu 1 5

- (2) INFORMATION FOR SEQ ID NO: 17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 Base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURES:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1..29

	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 17:			
CGCGGATCCG ARATNATNCC NCARAAYGT 29					
(2) INFORMATION FOR SEQ ID NO: 18:					
	(i) SEQUENCE CHARACTERISTICS (A) LENGTH: 7 Amino acid (B) TYPE: Amino acid (C) STRANDEDNESS: Singl (D) TOPOLOGY: linear	ds			
	(ii) MOLECULE TYPE: Protein				
	<pre>(ix) FEATURES: (A) NAME/KEY: Protein (B) LOCATION: 17</pre>				
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 18:			
	Glu Ile Ile Pro Gln Asn Val 1 5				
(2)	INFORMATION FOR SEQ ID NO: 19	:			
	(i) SEQUENCE CHARACTERISTICS (A) LENGTH: 29 Base pai (B) TYPE: Nucleic acid (C) STRANDEDNESS: Singl (D) TOPOLOGY: linear	cs			
	(ii) MOLECULE TYPE: DNA (geno	nic)			
	(ix) FEATURES: (A) NAME/KEY: exon (B) LOCATION: 129				
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 19:			
CCGC	GGAATTCT AYAARGAYGA RAAYGARTT		29		
(2)	INFORMATION FOR SEQ ID NO: 20	:			
	(i) SEQUENCE CHARACTERISTICS (A) LENGTH: 7 Amino aci (B) TYPE: Amino acid (C) STRANDEDNESS: Singl (D) TOPOLOGY: linear	ds			
	(ii) MOLECULE TYPE: Protein				
	<pre>(ix) FEATURES: (A) NAME/KEY: Protein (B) LOCATION: 17</pre>				
	(xi) SEQUENCE DESCRIPTION: SE	Q ID NO: 20:			

Tyr Lys Asp Glu Asn Glu Phe 1 5

- (2) INFORMATION FOR SEQ ID NO: 21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 Base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURES:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1..31
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AAAACTGCAG NGCRTCCATR AAYTCRTTYT C

31

- (2) INFORMATION FOR SEQ ID NO: 22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..7
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Asp Met Phe Glu Asn Glu

- (2) INFORMATION FOR SEQ ID NO: 23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 Base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURES:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1..31
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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- (2) INFORMATION FOR SEQ ID NO: 24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 Amino acids(B) TYPE: Amino acid

 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..7
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Lys Glu Glu Asn Ser Phe Val

- (2) INFORMATION FOR SEQ ID NO: 25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 Base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURES:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1..32
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACATGCATG TAGACGCACT TGGAGAAGAG GC

32

- (2) INFORMATION FOR SEQ ID NO: 26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (ix) FEATURES:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..8
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 - Val Asp Ala Leu Gly Glu Glu Ala

29	
(2) INFORMATION FOR SEQ ID NO: 27:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(ix) FEATURES: (A) NAME/KEY: exon (B) LOCATION: 136	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
CCGGAATTCC CTGAACAGTA CAGAGAGATC ATTCCA	36
(2) INFORMATION FOR SEQ ID NO: 28:	٠
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 Amino acids (B) TYPE: Amino acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Protein	
<pre>(ix) FEATURES: (A) NAME/KEY: Protein (B) LOCATION: 19</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:	
Pro Glu Gln Tyr Arg Glu Ile Ile Pro 1 5	
(2) INFORMATION FOR SEQ ID NO: 29:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 560 Base pairs (B) TYPE: Nucleic acid (C) STRANDEDNESS: Single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(ix) FEATURES: (A) NAME/KEY: exon (B) LOCATION: 1562	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:	
TGGAGAARTA CGAAGATATT CCTGAACAGT ACAGAGAGAT CATTCCACAA AACGTGGCCG	60
AGCATTTAAA ATCGATAACT CAGGAAGAGA AAAAAGTGCT CAAAGAATTT GTTAAAGACT	120
ATGCAAAATA CAAAGATGAA AATGAGTTCA TGGACGCATT AAAGCAAAAA TCTGAAAGCC	180

TTTATGAGAA	AGCTAAAAAA	CTTCAAGATT	TGCTGAAATC	AAAAGTAGAC	GCACTTGGAG	240
AAGAGGCAAA	ACAATTTGTG	ATGAAGCTTA	TCGCTGAGGC	TCGTAAATTC	CACGCAGAGC	300
TACTGGCCGG	CATCAAACCA	TCGCTAGAAG	AACTAAAAGC	CGTCGCTAAA	AAGCATATTG	360
AAGAGTTTGA	GAAGTTATCA	GATGCAGCTA	AAGATGATTT	CAAAAAGCAA	TTCCCTATCC	420
TCACATCCGT	GTTCAGCAAT	GAAAAAGCAA	AGAAAATGAT	GGACAACTTT	GTGAAAAATT	480
AAAGTTGTAT	GATTTGCAGG	ATATGAAATA	AATGTTAAAT	TGAAAAAAA	AAAAAAAA	540
AAAAAAAA	АААААААА	AG				562

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 Amino acids
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (ix) FEATURES:
 - (A) NAME/KEY: Protein
 (B) LOCATION: 1..159
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
- Glu Lys Tyr Glu Asp Ile Pro Glu Gln Tyr Arg Glu Ile Ile Pro Gln
 1 5 10 15
- Asn Val Ala Glu His Leu Lys Ser Ile Thr Glu Glu Glu Lys Lys Val 20 25 30
- Leu Lys Glu Phe Val Lys Asp Tyr Ala Lys Tyr Lys Asp Glu Asn Glu 35 40 45
- Phe Met Asp Ala Leu Lys Gln Lys Ser Glu Ser Leu Tyr Glu Lys Ala 50 55 60
- Lys Lys Leu Gln Asp Leu Leu Lys Ser Lys Val Asp Ala Leu Gly Glu 65 70 75 80
- Glu Ala Lys Gln Phe Val Met Lys Leu Ile Ala Glu Ala Arg Lys Phe 85 90 95
- His Ala Glu Leu Leu Ala Gly Ile Lys Pro Ser Leu Glu Glu Leu Lys 100 105 110
- Ala Val Ala Lys Lys His Ile Glu Glu Phe Glu Lys Leu Ser Asp Ala 115 120 125
- Ala Lys Asp Asp Phe Lys Lys Gln Phe Pro Ile Leu Thr Ser Val Phe 130 135 140